

CRF Processing Date: 12/31/2001  
Edited by: AW  
Verified by: AW (STIC sta)

Serial Number: 10/007,408

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEO ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEO ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: Seq 3 - corrected spelling of "amino"

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

#2

## RAW SEQUENCE LISTING

DATE: 12/31/2001

PATENT APPLICATION: US/10/007,408

TIME: 18:46:12

Input Set : A:\pto.amc.txt

Output Set: N:\CRF3\12312001\J007408.raw

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: WAKAMIYA, Nobutaka

8 (ii) TITLE OF INVENTION: RECOMBINANT CONGLUTININ AND PRODUCING

9 METHOD THEREOF

11 (iii) NUMBER OF SEQUENCES: 5

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

15 (B) STREET: 233 South Wacker Drive/6300 Sears Tower

16 (C) CITY: Chicago

17 (D) STATE: Illinois

18 (E) COUNTRY: United States of America

19 (F) ZIP: 60606-6402

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/007,408

C--> 29 (B) FILING DATE: 08-Nov-2001

30 (C) CLASSIFICATION:

36 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: PCT/JP95/02035

34 (B) FILING DATE: 02-OCT-1995

37 (A) APPLICATION NUMBER: JPA - 209698

38 (B) FILING DATE: 17-AUG-1995

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Gass, David A.

42 (B) REGISTRATION NUMBER: 38,153

43 (C) REFERENCE/DOCKET NUMBER: 19036/34546

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: (312) 474-6300

47 (B) TELEFAX: (312) 474-0448

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 351 amino acids

54 (B) TYPE: amino acid

55 (C) STRANDEDNESS: not relevant

58 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

67 Ala Glu Met Thr Thr Phe Ser Gln Lys Ile Leu Ala Asn Ala Cys Thr

68 1 5 10 15

70 Leu Val Met Cys Ser Pro Leu Glu Ser Gly Leu Pro Gly His Asp Gly

71 20 25 30

73 Gln Asp Gly Arg Glu Cys Pro His Gly Glu Lys Gly Asp Pro Gly Ser

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```

74          35          40          45
76  Pro Gly Pro Ala Gly Arg Ala Gly Arg Pro Gly Trp Val Gly Pro Ile
77          50          55          60
79  Gly Pro Lys Gly Asp Asn Gly Phe Val Gly Glu Pro Gly Pro Lys Gly
80          65          70          75          80
82  Asp Thr Gly Pro Arg Gly Pro Pro Gly Met Pro Gly Pro Ala Gly Arg
83          85          90          95
85  Glu Gly Pro Ser Gly Lys Gln Gly Ser Met Gly Pro Pro Gly Thr Pro
86          100          105          110
88  Gly Pro Lys Gly Glu Thr Gly Pro Lys Gly Gly Val Gly Ala Pro Gly
89          115          120          125
91  Ile Gln Gly Phe Pro Gly Pro Ser Gly Leu Lys Gly Glu Lys Gly Ala
92          130          135          140
94  Pro Gly Glu Thr Gly Ala Pro Gly Arg Ala Gly Val Thr Gly Pro Ser
95          145          150          155          160
97  Gly Ala Ile Gly Pro Gln Gly Pro Ser Gly Ala Arg Gly Pro Pro Gly
98          165          170          175
100  Leu Lys Gly Asp Arg Gly Asp Pro Gly Glu Thr Gly Ala Ser Gly Glu
101          180          185          190
103  Ser Gly Leu Ala Glu Val Asn Ala Leu Lys Gln Arg Val Thr Ile Leu
104          195          200          205
106  Asp Gly His Leu Arg Arg Phe Gln Asn Ala Phe Ser Gln Tyr Lys Lys
107          210          215          220
109  Ala Val Leu Phe Pro Asp Gly Gln Ala Val Gly Glu Lys Ile Phe Lys
110          225          230          235          240
113  Thr Ala Gly Ala Val Lys Ser Tyr Ser Asp Ala Glu Gln Leu Cys Arg
114          245          250          255
116  Glu Ala Lys Gly Gln Leu Ala Ser Pro Arg Ser Ser Ala Glu Asn Glu
117          260          265          270
119  Ala Val Thr Gln Met Val Arg Ala Gln Glu Lys Asn Ala Tyr Leu Ser
120          275          280          285
122  Met Asn Asp Ile Ser Thr Glu Gly Arg Phe Thr Tyr Pro Thr Gly Glu
123          290          295          300
125  Ile Leu Val Tyr Ser Asn Trp Ala Asp Gly Glu Pro Asn Asn Ser Asp
126          305          310          315          320
128  Glu Gly Gln Pro Glu Asn Cys Val Glu Ile Phe Pro Asp Gly Lys Trp
129          325          330          335
131  Asn Asp Val Pro Cys Ser Lys Gln Leu Leu Val Ile Cys Glu Phe
132          340          345          350

```

134 (2) INFORMATION FOR SEQ ID NO: 2:

136 (i) SEQUENCE CHARACTERISTICS:

137 (A) LENGTH: 171 amino acids

138 (B) TYPE: amino acid

139 (C) STRANDEDNESS: not relevant

140 (D) TOPOLOGY: linear

142 (ii) MOLECULE TYPE: protein

147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

149  Gly Leu Pro Gly His Asp Gly Gln Asp Gly Arg Glu Cys Pro His Gly
150  1          5          10          15

```

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```

152   Glu Lys Gly Asp Pro Gly Ser Pro Gly Pro Ala Gly Arg Ala Gly Arg
153           20           25           30
155   Pro Gly Trp Val Gly Pro Ile Gly Pro Lys Gly Asp Asn Gly Phe Val
156           35           40           45
158   Gly Glu Pro Gly Pro Lys Gly Asp Thr Gly Pro Arg Gly Pro Pro Gly
159           50           55           60
161   Met Pro Gly Pro Ala Gly Arg Glu Gly Pro Ser Gly Lys Gln Gly Ser
162           65           70           75           80
164   Met Gly Pro Pro Gly Thr Pro Gly Pro Lys Gly Glu Thr Gly Pro Lys
165           85           90           95
168   Gly Gly Val Gly Ala Pro Gly Ile Gln Gly Phe Pro Gly Pro Ser Gly
169           100          105          110
171   Leu Lys Gly Glu Lys Gly Ala Pro Gly Glu Thr Gly Ala Pro Gly Arg
172           115          120          125
174   Ala Gly Val Thr Gly Pro Ser Gly Ala Ile Gly Pro Gln Gly Pro Ser
175           130          135          140
177   Gly Ala Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Asp Pro Gly
178           145          150          155          160
180   Glu Thr Gly Ala Ser Gly Glu Ser Gly Leu Ala
181           165          170

```

183 (2) INFORMATION FOR SEQ ID NO: 3:

185 (i) SEQUENCE CHARACTERISTICS:

186 (A) LENGTH: 3 amino acids

187 (B) TYPE: amino acid

188 (C) STRANDEDNESS: not relevant

189 (D) TOPOLOGY: linear

191 (ii) MOLECULE TYPE: peptide

194 (ix) FEATURE:

195 (A) NAME/KEY: misc.

196 (B) LOCATION: 2

197 (D) OTHER INFORMATION: /note= "2ND amino acid is a  
198 protein-constituting amino acid."

200 (ix) FEATURE:

201 (A) NAME/KEY: misc.

202 (B) LOCATION: 3

203 (D) OTHER INFORMATION: /note= "3RD amino acid is a  
204 protein-constituting amino acid."

207 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

W--&gt; 209 Gly Xaa Xaa

210 1

212 (2) INFORMATION FOR SEQ ID NO: 4:

214 (i) SEQUENCE CHARACTERISTICS:

215 (A) LENGTH: 28 base pairs

216 (B) TYPE: nucleic acid

217 (C) STRANDEDNESS: single

218 (D) TOPOLOGY: linear

220 (ii) MOLECULE TYPE: other nucleic acid

221 (A) DESCRIPTION: /desc = "synthesized DNA"

226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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```
228 GGCTCGAGGG GGAGAGTGGG CTTGCAGA 28
230 (2) INFORMATION FOR SEQ ID NO: 5:
232 (i) SEQUENCE CHARACTERISTICS:
233 (A) LENGTH: 28 base pairs
234 (B) TYPE: nucleic acid
235 (C) STRANDEDNESS: single
236 (D) TOPOLOGY: linear
238 (ii) MOLECULE TYPE: other nucleic acid
239 (A) DESCRIPTION: /desc = "synthesized DNA"
244 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
246 GGGAATTCTC AAAACTCGCA GATCACAA 28
```

VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3